


```

QY      1 EREKE 5
      11111
Db      32 EREKE 36

RESULT 3
T01625
hypothetical protein At2g18970 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F19F24.17
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19 Feb 1999 #sequence_revision 19-Feb-1999 #text_change 16-Feb-2001
C:Accession: T01625; H84570
R:Rounsley, S.D.; Lin, X.; Kellum, K.A.; Crosby, M.L.; Brandon, E.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, April 1998
A:Description: Arabidopsis thaliana chromosome 11 BAC F19F24 genomic sequence.
A:Reference number: Z14153
A:Accession: T01625
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-62 <R0D>
A:Cross-references: EMBL:AF003673; NID:3304543; PID:g3004559
A:Experimental source: cultivar Columbia
K:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, E.D.; Fujii, J.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Mayam, L.; Taiton, L.;
cress, B.; Nierman, W.C.; White, G.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: BR4570
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <S10>
A:Cross-references: GR:AF002093; NID:g3004559; PIDN:AAC09032 1; GSPDB:GN00139
C:Genetics:
A:Gene: F19F24.17; At2g18970
A:Map position: 2
A:Intons: 11/2

Query Match      100.0%; Score 25; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EREKE 5
      11111
Db      53 EREKE 57

RESULT 4
T04546
hypothetical protein F2H12.160 Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999
R:Revan, M.; Gilbert, R.; Braum, M.; Holzer, E.; Brandt, A.; Guesstherheit, A.; Panetier,
submitted to the Protein Sequence Database, February 1998
A:Reference number: Z15377
A:Accession: T04546
A:Molecule type: DNA
A:Residues: 1-66 <BEV>
A:Cross-references: EMBL:AL021710
A:Experimental source: cultivar Columbia; BAC clone F2H12
C:Genetics:
A:Map position: 4
A:Intons: 17/1
A:Note: F2H12.160

Query Match      100.0%; Score 25; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EREKE 5
      11111
Db      50 EREKE 54

RESULT 7
A71836
hypothetical protein jhpl197 Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C:Accession: A71836
R:Alm, R.A.; Ling, L.S.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.;
Ives, C.; Gibson, R.; Morberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.P.
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p

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Db      19 EREKE 23

RESULT 5
S77762
hypothetical protein M0030 - Mycoplasma capricolum (treadment)
C:Species: Mycoplasma capricolum
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 21-Jul-2000
C:Accession: S77762; S48585
R:Bork, P.; Ouedenis, G.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert,
Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physi
A:Reference number: S77739; MUID:96059441; PMID:7476192
A:Accession: S77762
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-80 <HOR>
A:Cross-references: EMBL:Z33027; NID:341690; PIDN:CAAR3706.1; PID:04370129
A:Experimental source: ATCC 27343
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: GCC3

Query Match      100.0%; Score 25; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EREKE 5
      11111
Db      46 EREKE 50

RESULT 6
T50084
hypothetical coiled-coil protein [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
C:Accession: T50084
R:Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, H.G.
submitted to the EMBL Data Library, November 1999
A:Reference number: Z25035
A:Accession: T50084
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-111 <SAU>
A:Cross-references: EMBL:AL132984; PIDN:CAH61216.1; GSPDB:GN000066; SPDB:SPAC1556.05c
A:Experimental source: strain 972h(-); cosmid c1556
C:Genetics:
A:Gene: SPDB:SPAC1556.05c
A:Map position: 1
A:Intons: 12/1, 15/2, 64/3
C:Superfamily: Saccharomyces cerevisiae hypothetical protein YG1029w

Query Match      100.0%; Score 25; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 110+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EREKE 5
      11111
Db      50 EREKE 54

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A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: A71836
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-123 <ARN>
 A:Cross-references: GB:AF001546; GB:AF001439; NID:q4155799; PIRN:AA00706.1; PIR:q415580
 A:Experimental source: strain J99
 C:Genetics:
 C:Superfamily: Helicobacter pylori hypothetical protein jhp1157

Query Match 100.0%; Score 25; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 |||||
 DB 76 EREKE 80

RESULT 8

A86533
 Small protein B [imported] - Chlamydia pneumoniae (strain J138)
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 02 Mar 2001; #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: A86533
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
 Nucleic Acids Res. 28, 2111-2114, 2000
 A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: A86533
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-151 <STO>
 A:Cross-references: GB:RA000008; NID:q8978711; PIRN:BA098547.1; GSPDR:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: smph
 C:Superfamily: small protein smph

Query Match 100.0%; Score 25; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 |||||
 DB 135 EREKE 139

RESULT 9

C72090
 Small protein B - Chlamydia pneumoniae (strain CWL029)
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 23 Apr 1999; #sequence_revision 23-Apr-1999 #text_change 07-May-2000
 C:Accession: G72090
 R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, J.; Grimwood, J.
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis
 A:Reference number: A72000; MUID:59206666; PMID:18192488
 A:Accession: G72090
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-151 <ARN>
 A:Cross-references: GB:AF001518; GB:AF001439; NID:q4155799; PIRN:AA00706.1; PIR:q415580
 A:Experimental source: strain CWL029
 C:Genetics:
 A:Gene: smph
 C:Superfamily: small protein smph

Query Match 100.0%; Score 25; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 |||||
 DB 135 EREKE 139

RESULT 10

S01399
 H+transporting two-sector ATPase (EC 3.6.3.14) chain b precursor Thermophilic Bact
 C:Species: thermophilic bacterium PS-3
 C:Date: 10 Sep 1999; #sequence_revision 10-Sep-1999 #text_change 14-Dec-2001
 C:Accession: S01399
 R:Ohya, S.; Yoshida, M.; Ishizuka, M.; Hirata, H.; Hamada, Y.; Kawata-Hamada, Y.;
 Biochim. Biophys. Acta 933, 141-155, 1998
 A:Title: Sequence and over-expression of subunits of adenosine triphosphate synthase
 A:Reference number: S01397; MUID:88163679; PMID:2894854
 A:Accession: S01399
 A:Molecule type: DNA
 A:Residues: 1-163 <OH>
 A:Cross-references: PMB:X07804; NID:q45808; PIRN:CAA30650.1; PIR:q581473
 A:Note: part of this sequence, including the amino end of the mature protein, was con
 C:Genetics:
 A:Start codon: GTG
 C:Superfamily: H+transporting ATP synthase chain I
 C:Keywords: ATP biosynthesis, hydrolase, membrane associated complex, transmembrane p
 Eukaryotic, H+transporting ATP synthase chain b #status experimental

QY 1 EREKE 5
 |||||
 DB 125 EREKE 129

RESULT 11

H81578
 smph protein CP0421 [imported] - Chlamydia pneumoniae (strain AR39)
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 31-Mar-2000; #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
 C:Accession: H81578
 R:Prod, T.D.; Ruanham, P.C.; Shen, C.; Gill, S.P.; Hoidelberg, J.F.; White, G.; Hicke
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
 A:Reference number: A81500; MUID:20150265; PMID:10684935
 A:Accession: H81578
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-165 <REA>
 A:Cross-references: GB:AL002203; GB:AF002161; NID:q4189939; PIRN:AA18294.1; PIR:q418
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CP0421
 C:Superfamily: small protein smph

QY 1 EREKE 5
 |||||
 DB 149 EREKE 153

RESULT 12

G70436
 Hypothetical protein eq.1581 - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 02 May 1998; #sequence_revision 02-May-1998 #text_change 04-Mar-2000
 C:Accession: G70436
 R:Backert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; LeDoux, A.L.; Graham, D.E.;
 V.
 Query Match 100.0%; Score 25; DB 2; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 |||||
 DB 149 EREKE 153

Nature 392, 453-458, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70400; M11P-9a1g6666; PMID:9537320
 A:Accession: G70436
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-167 <GFA>
 A:Cross references: GB:AF000746; NID:g2983925; FIDN:AAC07489.1, FID:g2983940, GB:AE00069
 A:Experimental source: strain VF5
 A:Gene: aq1581
 A:Superfamily: Aquifex aeolicus hypothetical protein aq1581

Query Match 100.0%; Score 25; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 73 EREKE 77
 |||||

RESULT 14
 A11600
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27 Nov 2001 #text_change 27-Nov-2001
 C:Accession: A11600
 C:Glasser, P.; Franquell, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Hernandez, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Kist, U.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Mak, G.; Schluter, T.; Simoes, N.; Trier, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of Listeria species.
 A:Reference number: A11077; MUID:21537279; PMID:11679669
 A:Accession: A11600
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-168 <GIA>
 A:Cross references: GB:AL52022; FIDN:CA95577.1; FID:g16419819; GSEDB:GN00178
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lin1346

Query Match 100.0%; Score 25; DB 2; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 80 EREKE 84
 |||||

RESULT 14
 S45548
 A:Title: hypothetical protein ypuF - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-Jul-2000
 C:Accession: S45548; E69942
 C:Porokh, A.; Zumslein, E.; Azevedo, V.; Ehrlich, S.D.; Serrin, P.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S45543
 A:Accession: S45548
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-174 <SGR>
 A:Cross references: EMBL:U09228; NID:g410114; PIDN:AAA57486.1; PID:g410130
 R:Kunst, F.; Ogasawara, N.; Moser, J.; Altierini, A.M.; Alloni, G.; Azevedo, V.; Berti, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chao, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
 A:Authors: Fongor, J.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallon

tech, J.; Harwood, C.R.; Renaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.; Kottler, P.; Koningstein, G.; Krog, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete, R.; Rieker, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadai, Y.; Sato, T.; Seunl, A.; Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tojima, A.; Tosato, V.; Uchiya, T.; Winters, F.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.F.; Zumslein, E.; Yoshikawa, H.; Zumslein, A.; Yoshida, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: E69942
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-174 <KUN>
 A:Cross references: GB:AL009129, NID:q2634723, FIDN:CAA56239.1; PID:q587434
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ypuF
 A:Start codon: TTG
 C:Superfamily: Bacillus subtilis hypothetical protein ypuF

Query Match 100.0%; Score 25; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 161 EREKE 165
 |||||

RESULT 15
 S48795
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S48795
 R:Farza, H.
 submitted to the EMBL Data Library, June 1994
 A:Reference number: S48790
 A:Accession: S48795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-175 <FAR>
 A:Cross references: EMBL:X79859; NID:q587433; PIDN:CAA56239.1; PID:q587434
 C:Genetics:
 A:Introns: 14/2
 C:Superfamily: troponin T
 C:Keywords: cardiac muscle; heart

Query Match 100.0%; Score 25; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 139 EREKE 143
 |||||

Search completed: January 16, 2003, 16:57:46
 Job time: 11:23:33 sec